RAW SEQUENCE LISTING
PATENT APPLICATION *US/08/726,211*

INPUT SET: S13733.raw

This Raw Listing contains the General Information Section and up to the first 5 pages.

ENTERED

SEQUENCE LISTING

(1) General Information:

(i) APPLICANT: Tormo, Mar
Tari, Ana M.
Lopez-Berestein, Gabriel

(ii) TITLE OF INVENTION: INHIBITION OF Bcl-2 PROTEIN EXPRESSION BY LIPOSOMAL ANTISENSE OLIGODEOXYNUCLEOTIDES

(iii) NUMBER OF SEQUENCES: 7

(iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Arnold, White & Durkee
(B) STREET: P.O. Box 4433
(C) CITY: Houston
(D) STATE: Texas
(E) COUNTRY: United States of America
(F) ZIP: 77210

(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:
--> OK **(A) APPLICATION NUMBER: US Unknown**
(B) FILING DATE: Concurrently Herewith
--> OK **(C) CLASSIFICATION: Unknown**

(viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Wilson, Mark B.
(B) REGISTRATION NUMBER: 37,259
(C) REFERENCE/DOCKET NUMBER: UTXC:504

(ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: (512) 418-3000
(B) TELEFAX: (512) 474-7577

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CAGCGTGCGC CATCCTTC 18

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

ACGGTCCGCC ACTCCTTCCC 20

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CTGAAGGGCT TCTTCC 16

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5086 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1459..2175

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GCGCCCGCCC CTCCGCGCCG CCTGCCCGCC CGCCCGCCGC GCTCCCGCCC GCCGCTCTCC 60

GTGGCCCCGC CGCGCTGCCG CCGCCGCCGC TGCCAGCGAA GGTGCCGGGG CTCCGGGCCC 120

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101  TCCCTGCCGG CGGCCGTCAG CGCTCGGAGC GAACTGCGCG ACGGGAGGTC CGGGAGGCGA      180
102
103  CCGTAGTCGC GCCGCCGCGC AGGACCAGGA GGAGGAGAAA GGGTGCGCAG CCCGGAGGCG      240
104
105  GGGTGCGCCG GTGGGGTGCA GCGGAAGAGG GGGTCCAGGG GGGAGAACTT CGTAGCAGTC      300
106
107  ATCCTTTTTA GGAAAAGAGG GAAAAAATAA AACCCTCCCC CACCACCTCC TTCTCCCCAC      360
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109  CCCTCGCCGC ACCACACACA GCGCGGGCTT CTAGCGCTCG GCACCGGCGG GCCAGGCGCG      420
110
111  TCCTGCCTTC ATTTATCCAG CAGCTTTTCG GAAAATGCAT TTGCTGTTCG GAGTTTAATC      480
112
113  AGAAGACGAT TCCTGCCTCC GTCCCCGGCT CCTTCATCGT CCCATCTCCC CTGTCTCTCT      540
114
115  CCTGGGGAGG CGTGAAGCGG TCCCGTGGAT AGAGATTCAT GCCTGTGTCC GCGCGTGTGT      600
116
117  GCGCGCGTAT AAATTGCCGA GAAGGGGAAA ACATCACAGG ACTTCTGCGA ATACCGGACT      660
118
119  GAAAATTGTA ATTCATCTGC CGCCGCCGCT GCCAAAAAAA AACTCGAGCT CTTGAGATCT      720
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121  CCGGTTGGGA TTCCTGCGGA TTGACATTTC TGTGAAGCAG AAGTCTGGGA ATCGATCTGG      780
122
123  AAATCCTCCT AATTTTTACT CCCTCTCCCC CCGACTCCTG ATTCATTGGG AAGTTTCAAA      840
124
125  TCAGCTATAA CTGGAGAGTG CTGAAGATTG ATGGGATCGT TGCCTTATGC ATTTGTTTTG      900
126
127  GTTTTACAAA AAGGAAACTT GACAGAGGAT CATGCTGTAC TTAAAAAATA CAAGTAAGTC      960
128
129  TCGCACAGGA AATTGGTTTA ATGTAACTTT CAATGGAAAC CTTTGAGATT TTTTACTTAA     1020
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131  AGTGCATTCG AGTAAATTTA ATTTCCAGGC AGCTTAATAC ATTGTTTTTA GCCGTGTTAC     1080
132
133  TTGTAGTGTG TATGCCCTGC TTTCACTCAG TGTGTACAGG GAAACGCACC TGATTTTTTA     1140
134
135  CTTATTAGTT TGTTTTTTCT TTAACCTTTC AGCATCACAG AGGAAGTAGA CTGATATTAA     1200
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137  CAATACTTAC TAATAATAAC GTGCCTCATG AAATAAAGAT CCGAAAGGAA TTGGAATAAA     1260
138
139  AATTTCCTGC GTCTCATGCC AAGAGGGAAA CACCAGAATC AAGTGTTCCG CGTGATTGAA     1320
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141  GACACCCCCT CGTCCAAGAA TGCAAAGCAC ATCCAATAAA ATAGCTGGAT TATAACTCCT     1380
142
143  CTTCTTTCTC TGGGGGCCGT GGGGTGGGAG CTGGGGCGAG AGGTGCCGTT GGCCCCCGTT     1440
144
145  GCTTTTCCTC TGGGAAGG ATG GCG CAC GCT GGG AGA ACG GGG TAC GAC AAC        1491
146                     Met Ala His Ala Gly Arg Thr Gly Tyr Asp Asn
147                       1               5                  10
148
149  CGG GAG ATA GTG ATG AAG TAC ATC CAT TAT AAG CTG TCG CAG AGG GGC        1539
150  Arg Glu Ile Val Met Lys Tyr Ile His Tyr Lys Leu Ser Gln Arg Gly
151              15                  20                  25
152
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153  TAC GAG TGG GAT GCG GGA GAT GTG GGC GCC GCG CCC CCG GGG GCC GCC      1587
154  Tyr Glu Trp Asp Ala Gly Asp Val Gly Ala Ala Pro Pro Gly Ala Ala
155            30                  35                  40
156
157  CCC GCA CCG GGC ATC TTC TCC TCC CAG CCC GGG CAC ACG CCC CAT CCA      1635
158  Pro Ala Pro Gly Ile Phe Ser Ser Gln Pro Gly His Thr Pro His Pro
159       45                  50                  55
160
161  GCC GCA TCC CGC GAC CCG GTC GCC AGG ACC TCG CCG CTG CAG ACC CCG      1683
162  Ala Ala Ser Arg Asp Pro Val Ala Arg Thr Ser Pro Leu Gln Thr Pro
163   60                  65                  70                  75
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165  GCT GCC CCC GGC GCC GCC GCG GGG CCT GCG CTC AGC CCG GTG CCA CCT      1731
166  Ala Ala Pro Gly Ala Ala Ala Gly Pro Ala Leu Ser Pro Val Pro Pro
167                  80                  85                  90
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169  GTG GTC CAC CTG GCC CTC CGC CAA GCC GGC GAC GAC TTC TCC CGC CGC      1779
170  Val Val His Leu Ala Leu Arg Gln Ala Gly Asp Asp Phe Ser Arg Arg
171              95                  100                 105
172
173  TAC CGC GGC GAC TTC GCC GAG ATG TCC AGC CAG CTG CAC CTG ACG CCC      1827
174  Tyr Arg Gly Asp Phe Ala Glu Met Ser Ser Gln Leu His Leu Thr Pro
175          110                 115                 120
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177  TTC ACC GCG CGG GGA CGC TTT GCC ACG GTG GTG GAG GAG CTC TTC AGG      1875
178  Phe Thr Ala Arg Gly Arg Phe Ala Thr Val Val Glu Glu Leu Phe Arg
179      125                 130                 135
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181  GAC GGG GTG AAC TGG GGG AGG ATT GTG GCC TTC TTT GAG TTC GGT GGG      1923
182  Asp Gly Val Asn Trp Gly Arg Ile Val Ala Phe Phe Glu Phe Gly Gly
183  140                 145                 150                 155
184
185  GTC ATG TGT GTG GAG AGC GTC AAC CGG GAG ATG TCG CCC CTG GTG GAC      1971
186  Val Met Cys Val Glu Ser Val Asn Arg Glu Met Ser Pro Leu Val Asp
187                  160                 165                 170
188
189  AAC ATC GCC CTG TGG ATG ACT GAG TAC CTG AAC CGG CAC CTG CAC ACC      2019
190  Asn Ile Ala Leu Trp Met Thr Glu Tyr Leu Asn Arg His Leu His Thr
191              175                 180                 185
192
193  TGG ATC CAG GAT AAC GGA GGC TGG GAT GCC TTT GTG GAA CTG TAC GGC      2067
194  Trp Ile Gln Asp Asn Gly Gly Trp Asp Ala Phe Val Glu Leu Tyr Gly
195          190                 195                 200
196
197  CCC AGC ATG CGG CCT CTG TTT GAT TTC TCC TGG CTG TCT CTG AAG ACT      2115
198  Pro Ser Met Arg Pro Leu Phe Asp Phe Ser Trp Leu Ser Leu Lys Thr
199      205                 210                 215
200
201  CTG CTC AGT TTG GCC CTG GTG GGA GCT TGC ATC ACC CTG GGT GCC TAT      2163
202  Leu Leu Ser Leu Ala Leu Val Gly Ala Cys Ile Thr Leu Gly Ala Tyr
203  220                 225                 230                 235
204
205  CTG AGC CAC AAG TGAAGTCAAC ATGCCTGCCC CAAACAAATA TGCAAAAGGT          2215
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206 Leu Ser His Lys
207
208
209 TCACTAAAGC AGTAGAAATA ATATGCATTG TCAGTGATGT ACCATGAAAC AAAGCTGCAG 2275
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211 GCTGTTTAAG AAAAAATAAC ACACATATAA ACATCACACA CACAGACAGA CACACACACA 2335
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213 CACAACAATT AACAGTCTTC AGGCAAAACG TCGAATCAGC TATTTACTGC CAAAGGGAAA 2395
214
215 TATCATTTAT TTTTTACATT ATTAAGAAAA AAGATTTATT TATTTAAGAC AGTCCCATCA 2455
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217 AAACTCCGTC TTTGGAAATC CGACCACTAA TTGCCAAACA CCGCTTCGTG TGGCTCCACC 2515
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219 TGGATGTTCT GTGCCTGTAA ACATAGATTC GCTTTCCATG TTGTTGGCCG GATCACCATC 2575
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221 TGAAGAGCAG ACGGATGGAA AAAGGACCTG ATCATTGGGG AAGCTGGCTT TCTGGCTGCT 2635
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223 GGAGGCTGGG GAGAAGGTGT TCATTCACTT GCATTTCTTT GCCCTGGGGG CGTGATATTA 2695
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225 ACAGAGGGAG GGTTCCCGTG GGGGGAAGTC CATGCCTCCC TGGCCTGAAG AAGAGACTCT 2755
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227 TTGCATATGA CTCACATGAT GCATACCTGG TGGGAGGAAA AGAGTTGGGA ACTTCAGATG 2815
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229 GACCTAGTAC CCACTGAGAT TTCCACGCCG AAGGACAGCG ATGGGAAAAA TGCCCTTAAA 2875
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231 TCATAGGAAA GTATTTTTTT AAGCTACCAA TTGTGCCGAG AAAAGCATTT TAGCAATTTA 2935
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233 TACAATATCA TCCAGTACCT TAAACCCTGA TTGTGTATAT TCATATATTT TGGATACGCA 2995
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235 CCCCCCAACT CCCAATACTG GCTCTGTCTG AGTAAGAAAC AGAATCCTCT GGAACTTGAG 3055
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237 GAAGTGAACA TTTCGGTGAC TTCCGATCAG GAAGGCTAGA GTTACCCAGA GCATCAGGCC 3115
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239 GCCACAAGTG CCTGCTTTTA GGAGACCGAA GTCCGCAGAA CCTACCTGTG TCCCAGCTTG 3175
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241 GAGGCCTGGT CCTGGAACTG AGCCGGGCCC TCACTGGCCT CCTCCAGGGA TGATCAACAG 3235
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243 GGTAGTGTGG TCTCCGAATG TCTGGAAGCT GATGGATGGA GCTCAGAATT CCACTGTCAA 3295
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245 GAAAGAGCAG TAGAGGGGTG TGGCTGGGCC TGTCACCCTG GGGCCCTCCA GGTAGGCCCG 3355
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247 TTTTCACGTG GAGCATAGGA GCCACGACCC TTCTTAAGAC ATGTATCACT GTAGAGGGAA 3415
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249 GGAACAGAGG CCCTGGGCCT TCCTATCAGA AGGACATGGT GAAGGCTGGG AACGTGAGGA 3475
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251 GAGGCAATGG CCACGGCCCA TTTTGGCTGT AGCACATGGC ACGTTGGCTG TGTGGCCTTG 3535
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253 GCCACCTGTG AGTTTAAAGC AAGGCTTTAA ATGACTTTGG AGAGGGTCAC AAATCCTAAA 3595
254
255 AGAAGCATTG AAGTGAGGTG TCATGGATTA ATTGACCCCT GTCTATGGAA TTACATGTAA 3655
256
257 AACATTATCT TGTCACTGTA GTTTGGTTTT ATTTGAAAAC CTGACAAAAA AAAAGTTCCA 3715
258